## **CLAIMS**

- 1. A method of transforming trees to modify the fibre characteristics in trees, the method comprising stably incorporating into the plant genome a chimaeric gene comprising a promoter and a nucleic acid coding sequence encoding a gene capable of modifying the extension of fibre cell walls, and regenerating a plant having an altered genome.
- 2. A method according to Claim 1, wherein said nucleic acid sequence encodes one or more of the class of proteins known as expansins.
- 3. A method according to Claim 1 or 2, wherein said nucleic acid sequence is derived from Eucalyptus or cucumber.
- 4. A method according to Claim 3, wherein said nucleic acid sequence is one or more of SEQ. ID. Nos. 1-6 hereof or the cucumber expansin sequence known herein as cucumber Ex29 (GenBank Accession No. U30382), or a sequence which has sufficient homology to hybridise to any one of SEQ. ID. Nos. 1-6 or cucumber Ex29 under medium stringency conditions (washing at 2x SSC at 65°C).
- 5. A method according to any one of the preceding claims, wherein said nucleic acid sequence is an mRNA, a cDNA sequence or a genomic DNA.

- 6. A method according to any one of Claims 1-5, wherein said chimaeric gene is in accordance with any one of Claims 8-13.
- 7. A nucleic acid coding sequence encoding a gene capable of modifying the extension of fibre cell walls, the nucleic acid coding sequence being one or more of SEQ. ID. Nos. 1-6 hereof, or a sequence which has sufficient homology to hybridise to any one of SEQ. ID. Nos. 1-6 under medium stringency conditions.
- 8. A chimaeric gene comprising a promoter and a nucleic acid sequence encoding a gene capable of modifying the extension of fibre cell walls, said nucleic acid sequence being one or more of SEQ. ID. Nos. 1-6 hereof, or a sequence which has sufficient homology to hybridise thereto under medium stringency conditions.
- 9. A chimaeric gene according to Claim 6 for 8, wherein said chimaeric gene further comprises a terminator.
- 10. A chimaeric gene according to Claim 6, 8 or 9, wherein said chimaeric gene comprises said nucleic acid coding sequence as said nucleic acid sequence exists in nature, complete with endogenous promoter, terminator, introns and other regulatory sequences.
- 11. A chimaeric gene according to Claim 6, 8 or 9, wherein said chimaeric gene comprises said nucleic acid coding sequence, with or without introns, combined with a

heterologous promoter, terminator and/or other regulatory sequences.

- 12. A chimaeric gene according to any one of Claims 6 or 811, wherein said promoter is one of said group consisting
  of the cauliflower mosaic virus 35S promoter (CaMV35S),
  the cauliflower mosaic virus 19S promoter (CaMV19S), the
  nopaline synthase promoter, the rolc, patatin or petE
  promoters, or the AlcR/AlcS promoter.
- 13. A chimaeric gene according to any one of Claims 6 or 812, wherein said nucleic acid sequence, or parts thereof,
  is arranged in the normal reading frame direction or in
  the reverse reading frame direction.
- 14. A tree comprising a chimaeric gene according to any one of Claims 8-13.
- 15. A plant cell comprising a chimaeric gene according to any one of Claims 8-13.
- 16. A tree transformed according to the method of any one of Claims 1-7:
- 17. A tree according to Claim 16, said tree being a eucalypt, aspen, pine or larch.
- 18. A seed of a tree transformed according to the method of any one of Claims 1-7.